SEQ ID NO:1

FIGURE 1

CCGCGAGGTGCGCGGTCTCTTTAAGGCGGGTCCTGGTGGTTTCTGTTTCCTGAAGGA
AGTGACGGGGGGTGGATTGAATGAAAAGTGCAAAACACAGGCTCGCAGCGCTGGA
GCCCGGGGCCGCGGAGCCGGGCCGGGGCAGCGCCGTCTCCGCCTCGGGGCCGCCGG
GGGCGCCCTGCTGAGCGCTACCCACGTGCGTCCGCGCCACCTCGCGGGCGACCCCG
CGGCCAAGGCCCCCGGCGGAGCGGCTCCCGGGCGCCCCGAACTAGCCCCCAACTTT
GGGCGAAGTTTGCCTGCGCCTCTCCCCGCCCCCACGCGGCGCGCCGGGGCCGCGGA
CGGCAGCGGCCCCCGGGGATGCGCCTTCCCGGGGTACCCCTGGCGCGCCCTGCGCT
GCTGCTGCTGCTGCCGCTGCTCGCGCCGCTGCTGGGAACGGGTGCGCCGGCCGAGCT
GCGGGTCCGCGTGCGGCTGCCGGACGGCCAGGTGACCGAGGAGAGCCTGCAGGCGG
ACAGCGACGCGGACAGCATCAGCCTCGAGCTGCGCAAGCCCGACGGCACCCTCGTC
TCCTTCACCGCCGACTTCAAGAAGGATGTGAAGGTCTTCCGGGCCCTGATCCTGGGG
GAGCTGGAGAAGGGGCAGAGTCAGTTCCAGGCCCTCTGCTTTGTCACCCAGCTGCA
GCACAATGAGATCATCCCCAGTGAGGCCATGGCCAAGCTCCGGCAGAAAAATCCCC
GGGCAGTGCGGCAGGCGGAGGAGGTTCGGGGTCTGGAGCATCTGCACATGGATGTC
GCTGTCAACTTCAGCCAGGGGGCCCTGCTGAGCCCCCATCTCCACAACGTGTGTGCC
GAGGCCGTGGATGCCATCTACACCCGCCAGGAGGATGTCCGGTTCTGGCTGGAGCA
AGGTGTGGACAGTTCTGTGTTCGAGGCTCTGCCCAAGGCCTCAGAGCAGGCGGAGC
TGCCTCGCTGCAGGCAGGTGGGGGACCGCGGGAAGCCCTGCGTCTGCCACTATGGC
CTGAGCCTGGCCTGGTACCCCTGCATGCTCAAGTACTGCCACAGCCGCGACCGGCCC
ACGCCCTACAAGTGTGGCATCCGCAGCTGCCAGAAGAGCTACAGCTTCGACTTCTAC
GTGCCCCAGAGGCAGCTGTGTCTCTGGGATGAGGATCCCTACCCAGGCTAGGGTGG
GAGCAACCTGGGCGGGTGGCTGCTCTGGGCCCACTGCTCTTCACCAGCCACTAGAGG
GGGTGGCAACCCCCACCTGAGGCCTTATTTCCCTCCCTCCCCACTCCCCTGGCCCTA
GAGCCTGGGCCCCTCTGGCCCCATCTCACATGACTGTGAAGGGGGTGTGGCATGGCA
GGGGGTCTCATGAAGGCACCCCCATTCCCACCCTGTGCCTTCCTTGCGGGCAGAGAG
GGAGAGAAGGGCTCCCCAGATCTACACCCCTCCCTCCTGCATCTCCCCTGGAGTGTT
CACTTGCAAGCTGCCAAAACATGATGGCCTCTGGTTGTTCTGTTGAACTCCTTGAAC
GTTTAGACCCTAAAAGGAGTCTATACCTGGACACCCACCTCCCCAGACACAACTCCC
TTCCCCATGCACACATCTGGAAGGAGCTGGCCCCTCAGTCCCTTCCTACTCCCCAAC
AAGGGGCTCACTATCCCCAAAGAAGGAGCTGTTGGGGACCCACGACGCAGCCCCTG
TACTGGATTACAGCATATTCTCATCTCTGGCCCCGAGGCTGCCTGTGGGGCGAGTGG
AGACCTCCCATCACTGAGACAGATCACAGACCACGAGTGCCTTTCCCGGACCTGGAC
GTTGCCTCCAAAACAGGCACCAGCTCTTTCCCTCTCTAGACAGAAATATTTTTGTAA
GGTTCTGGGGCAGGGAGGGAGCATGAAGTACGAGGAAAACTTGAATTCCAGATTTT
TAATGCAAAGTATTTATCATTTCTACCAGAAATAAACGTTTTAAGTTTTTACTTGACT
AATGAGACCCAGAGTTTGGAGAAAACTTTTGGCCAATGCTGCCACCTGATGTCAGA
AAGTGTCCCCACACCCTAGCAGTGGCCTATCTTGGAACAAGAACTTCGAAAGCACCT

FIGURE 1 (continued)

ACTGTGTGCTCAGCCATTTGAGGAAGGAAGGAGGAGAAGGAAGATGTTACTAGGGA
AGGATGAGATAAAACTTCTGCACCCAAGACAATGAGACAGACATAACTGCAACCGT
AGTAAGCCAGTCAGAAATAGCCAGCGCGAAGGCAAGAGATGGGGTGGAGATTGGA
ACCCCGCTTCAGATCTGGGCTCGGCTACTTACCTGCTGTGCAGCCATGGGTCAAGTT
GCTTGACCTCTCTGTGCCTCCACTCCCTTAGCTATAAAATGAGCTTACTT

SEQ ID NO:2

FIGURE 2

MRLPGVPLARPALLLLLPLLAPLLGTGAPAELRVRVRLPDGQVTEESLQADSDADSISLEL
RKPDGTLVSFTADFKKDVKVFRALILGELEKGQSQFQALCFVTQLQHNEIIPSEAMAKLR
QKNPRAVRQAEEVRGLEHLHMDVAVNFSQGALLSPHLHNVCAEAVDAIYTRQEDVRF
WLEQGVDSSVFEALPKASEQAELPRCRQVGDRGKPCVCHYGLSLAWYPCMLKYCHSR
DRPTPYKCGIRSCQKSYSFDFYVPQRQLCLWDEDPYPG*

SEQ ID NO:3

FIGURE 3

MRLPGVPLARPALLLLLPLLAPLLG TGAPA

FIGURE 4

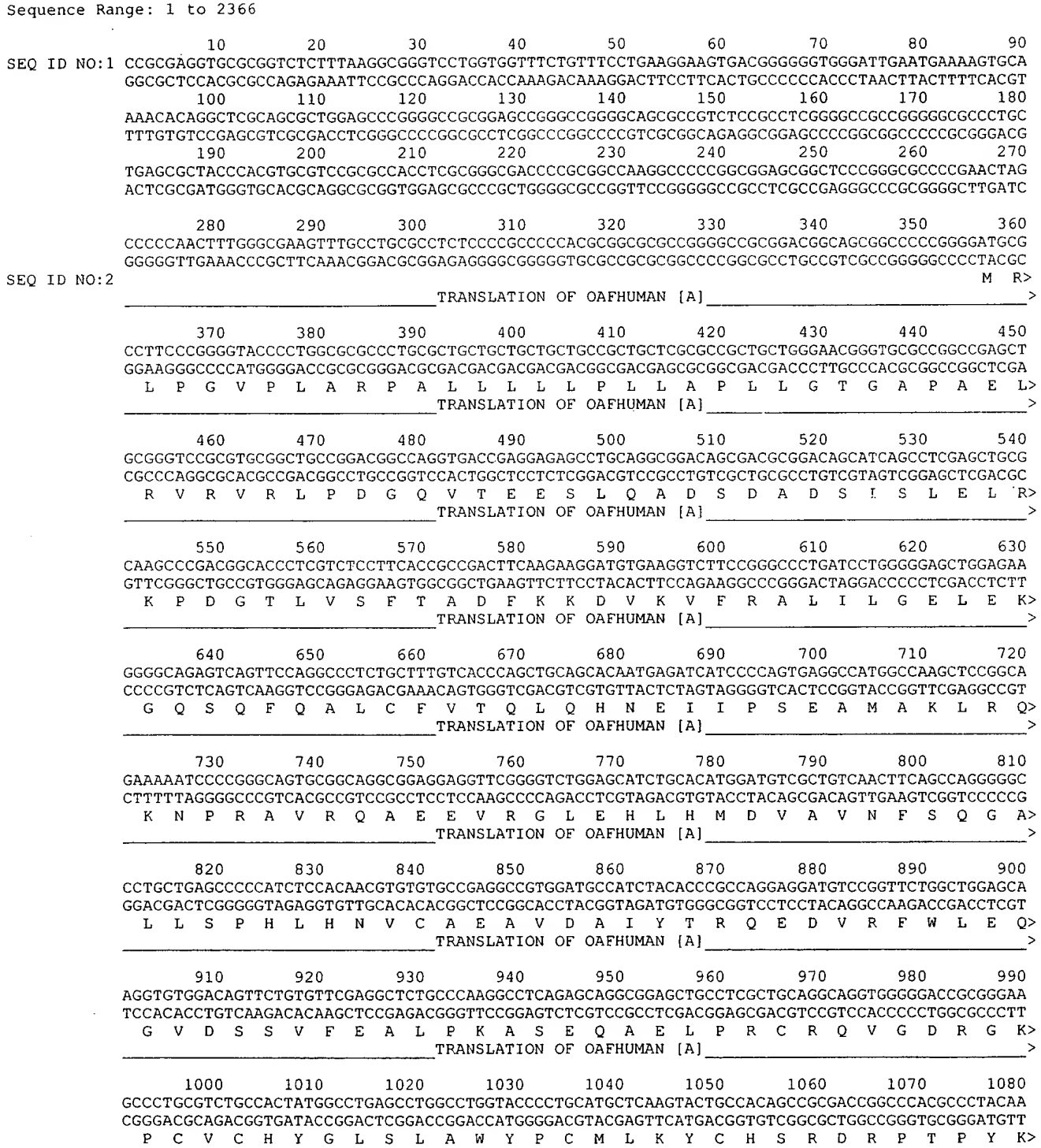

Sequence Range: 1 to 2366
SEQ ID NO:1
SEQ ID NO:2
TRANSLATION OF OAFHUMAN [A]

FIGURE 4 (continued)

```
_______________________________TRANSLATION OF OAFHUMAN [A]________________________________>

      1090      1100      1110      1120      1130      1140      1150      1160      1170
GTGTGGCATCCGCAGCTGCCAGAAGAGCTACAGCTTCGACTTCTACGTGCCCCAGAGGCAGCTGTGTCTCTGGGATGAGGATCCCTACCC
CACACCGTAGGCGTCGACGGTCTTCTCGATGTCGAAGCTGAAGATGCACGGGGTCTCCGTCGACACAGAGACCCTACTCCTAGGGATGGG
 C  G  I  R  S  C  Q  K  S  Y  S  F  D  F  Y  V  P  Q  R  Q  L  C  L  W  D  E  D  P  Y  P>
_______________________________TRANSLATION OF OAFHUMAN [A]________________________________>

      1180      1190      1200      1210      1220      1230      1240      1250      1260
AGGCTAGGGTGGGAGCAACCTGGGCGGGTGGCTGCTCTGGGCCCACTGCTCTTCACCAGCCACTAGAGGGGGTGGCAACCCCCACCTGAG
TCCGATCCCACCCTCGTTGGACCCGCCCACCGACGAGACCCGGGTGACGAGAAGTGGTCGGTGATCTCCCCCACCGTTGGGGGTGGACTC
 G  *

      1270      1280      1290      1300      1310      1320      1330      1340      1350
GCCTTATTTCCCTCCCTCCCCACTCCCCTGGCCCTAGAGCCTGGGCCCCTCTGGCCCCATCTCACATGACTGTGAAGGGGGTGTGGCATG
CGGAATAAAGGGAGGGAGGGGTGAGGGGACCGGGATCTCGGACCCGGGGAGACCGGGGTAGAGTGTACTGACACTTCCCCCACACCGTAC

      1360      1370      1380      1390      1400      1410      1420      1430      1440
GCAGGGGGTCTCATGAAGGCACCCCCATTCCCACCCTGTGCCTTCCTTGCGGGCAGAGAGGGAGAGAAGGGCTCCCCAGATCTACACCCC
CGTCCCCCAGAGTACTTCCGTGGGGGTAAGGGTGGGACACGGAAGGAACGCCCGTCTCTCCCTCTCTTCCCGAGGGGTCTAGATGTGGGG

      1450      1460      1470      1480      1490      1500      1510      1520      1530
TCCCTCCTGCATCTCCCCTGGAGTGTTCACTTGCAAGCTGCCAAAACATGATGGCCTCTGGTTGTTCTGTTGAACTCCTTGAACGTTTAG
AGGGAGGACGTAGAGGGGACCTCACAAGTGAACGTTCGACGGTTTTGTACTACCGGAGACCAACAAGACAACTTGAGGAACTTGCAAATC

      1540      1550      1560      1570      1580      1590      1600      1610      1620
ACCCTAAAAGGAGTCTATACCTGGACACCCACCTCCCCAGACACAACTCCCTTCCCCATGCACACATCTGGAAGGAGCTGGCCCCTCAGT
TGGGATTTTCCTCAGATATGGACCTGTGGGTGGAGGGGTCTGTGTTGAGGGAAGGGGTACGTGTGTAGACCTTCCTCGACCGGGGAGTCA

      1630      1640      1650      1660      1670      1680      1690      1700      1710
CCCTTCCTACTCCCCAACAAGGGGCTCACTATCCCCAAAGAAGGAGCTGTTGGGGACCCACGACGCAGCCCCTGTACTGGATTACAGCAT
GGGAAGGATGAGGGGTTGTTCCCCGAGTGATAGGGGTTTCTTCCTCGACAACCCCTGGGTGCTGCGTCGGGGACATGACCTAATGTCGTA

       1720      1730      1740      1750      1760      1770      1780      1790      1800
ATTCTCATCTCTGGCCCCGAGGCTGCCTGTGGGGCGAGTGGAGACCTCCCATCACTGAGACAGATCACAGACCACGAGTGCCTTTCCCGG
TAAGAGTAGAGACCGGGGCTCCGACGGACACCCCGCTCACCTCTGGAGGGTAGTGACTCTGTCTAGTGTCTGGTGCTCACGGAAAGGGCC

      1810      1820      1830      1840      1850      1860      1870      1880      1890
ACCTGGACGTTGCCTCCAAAACAGGCACCAGCTCTTTCCCTCTCTAGACAGAAATATTTTTGTAAGGTTCTGGGGCAGGGAGGGAGCATG
TGGACCTGCAACGGAGGTTTTGTCCGTGGTCGAGAAAGGGAGAGATCTGTCTTTATAAAAACATTCCAAGACCCCGTCCCTCCCTCGTAC

      1900      1910      1920      1930      1940      1950      1960      1970      1980
AAGTACGAGGAAAACTTGAATTCCAGATTTTTAATGCAAAGTATTTATCATTTCTACCAGAAATAAACGTTTAAGTTTTTACTTGACTA
TTCATGCTCCTTTTGAACTTAAGGTCTAAAAATTACGTTTCATAAATAGTAAAGATGGTCTTTATTTGCAAAATTCAAAAATGAACTGAT

      1990      2000      2010      2020      2030      2040      2050      2060      2070
ATGAGACCCAGAGTTTGGAGAAAACTTTTGGCCAATGCTGCCACCTGATGTCAGAAAGTGTCCCCACACCCTAGCAGTGGCCTATCTTGG
TACTCTGGGTCTCAAACCTCTTTTGAAAACCGGTTACGACGGTGGACTACAGTCTTTCACAGGGGTGTGGGATCGTCACCGGATAGAACC

      2080      2090      2100      2110      2120      2130      2140      2150      2160
AACAAGAACTTCGAAAGCACCTACTGTGTGCTCAGCCATTTGAGGAAGGAAGGAGGAGAAGGAAGATGTTACTAGGGAAGGATGAGATAA
TTGTTCTTGAAGCTTTCGTGGATGACACACGAGTCGGTAAACTCCTTCCTTCCTCCTCTTCCTTCTACAATGATCCCTTCCTACTCTATT

      2170      2180      2190      2200      2210      2220      2230      2240      2250
AACTTCTGCACCCAAGACAATGAGACAGACATAACTGCAACCGTAGTAAGCCAGTCAGAAATAGCCAGCGCGAAGGCAAGAGATGGGGTG
TTGAAGACGTGGGTTCTGTTACTCTGTCTGTATTGACGTTGGCATCATTCGGTCAGTCTTTATCGGTCGCGCTTCCGTTCTCTACCCCAC

      2260      2270      2280      2290      2300      2310      2320      2330      2340
GAGATTGGAACCCCGCTTCAGATCTGGGCTCGGCTACTTACCTGCTGTGCAGCCATGGGTCAAGTTGCTTGACCTCTCTGTGCCTCCACT
CTCTAACCTTGGGGCGAAGTCTAGACCCGAGCCGATGAATGGACGACACGTCGGTACCCAGTTCAACGAACTGGAGAGACACGGAGGTGA
   2350      2360
CCCTTAGCTATAAAATGAGCTTACTT
GGGAATCGATATTTTACTCGAATGAA
```

FIGURE 5

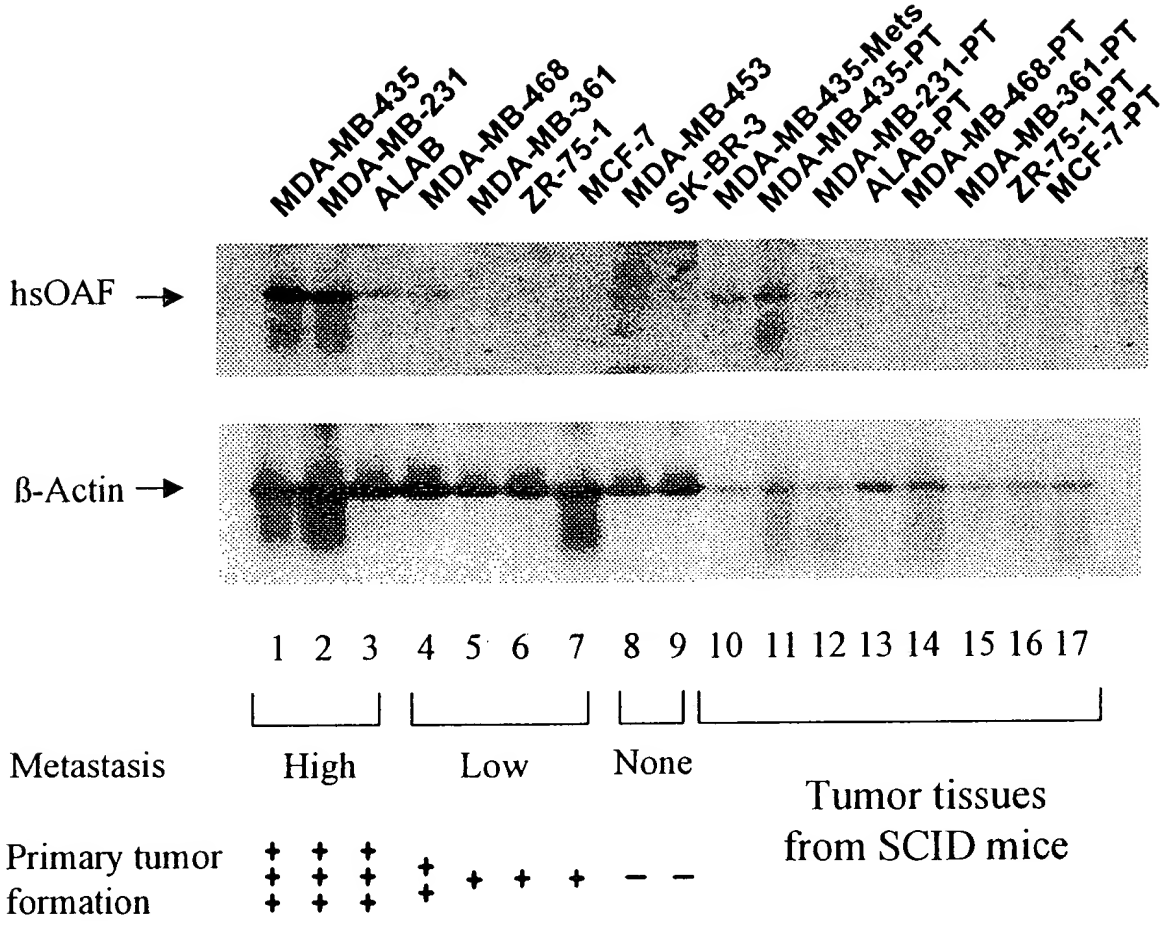

MDA-MB-435
MDA-MB-231
ALAB
MDA-MB-468
MDA-MB-361
ZR-75-1
MCF-7
MDA-MB-453
SK-BR-3
MDA-MB-435-Mets
MDA-MB-435-PT
MDA-MB-231-PT
ALAB-PT
MDA-MB-468-PT
MDA-MB-361-PT
ZR-75-1-PT
MCF-7-PT
hsOAF
ß-Actin
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17
Metastasis
High
Low
None
Tumor tissues from SCID mice
Primary tumor formation

FIGURE 6

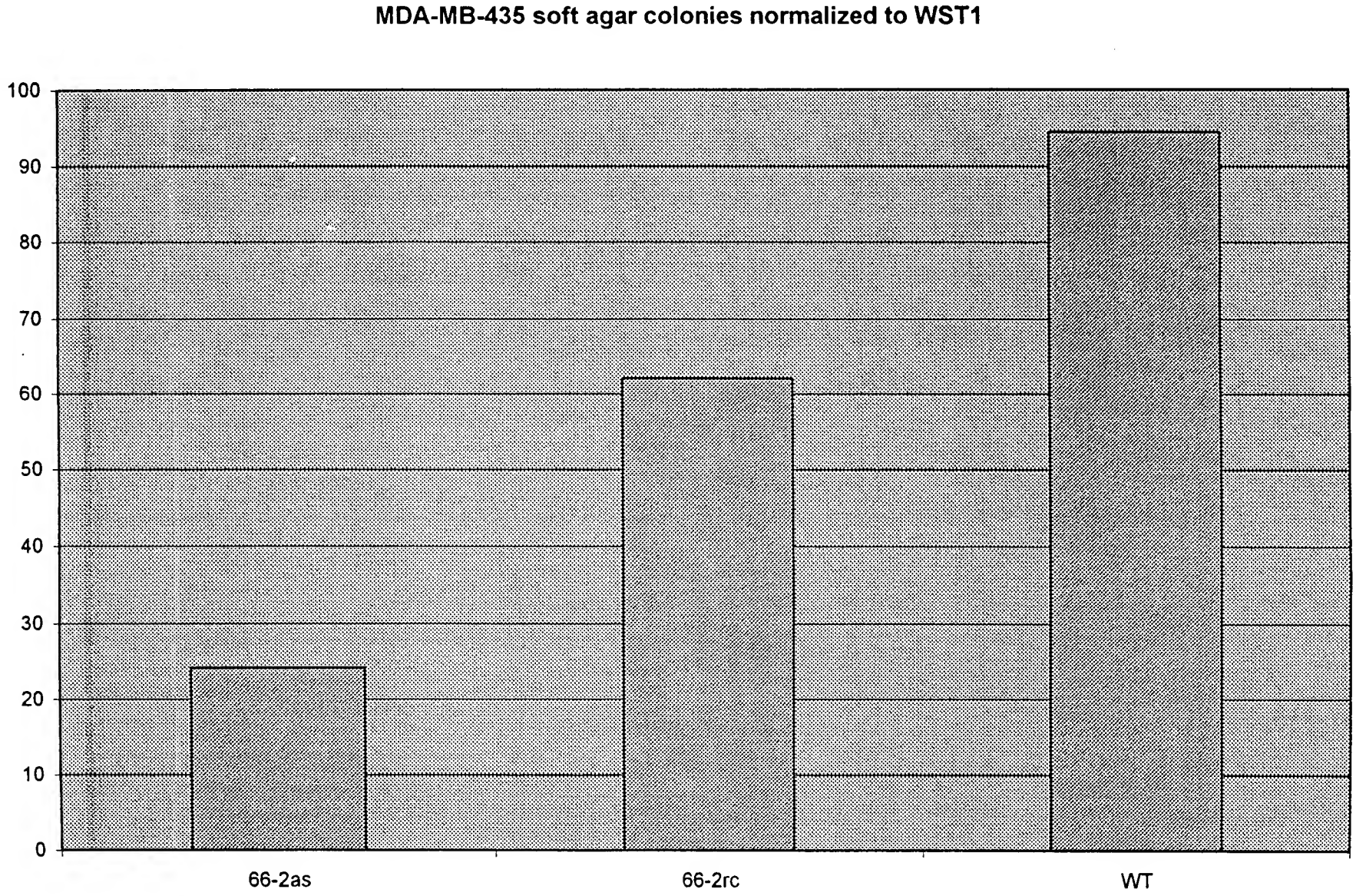

MDA-MB-435 soft agar colonies normalized to WST1
100
90
80
70
60
50
40
30
20
10
0
66-2as
66-2rc
WT

FIGURE 7

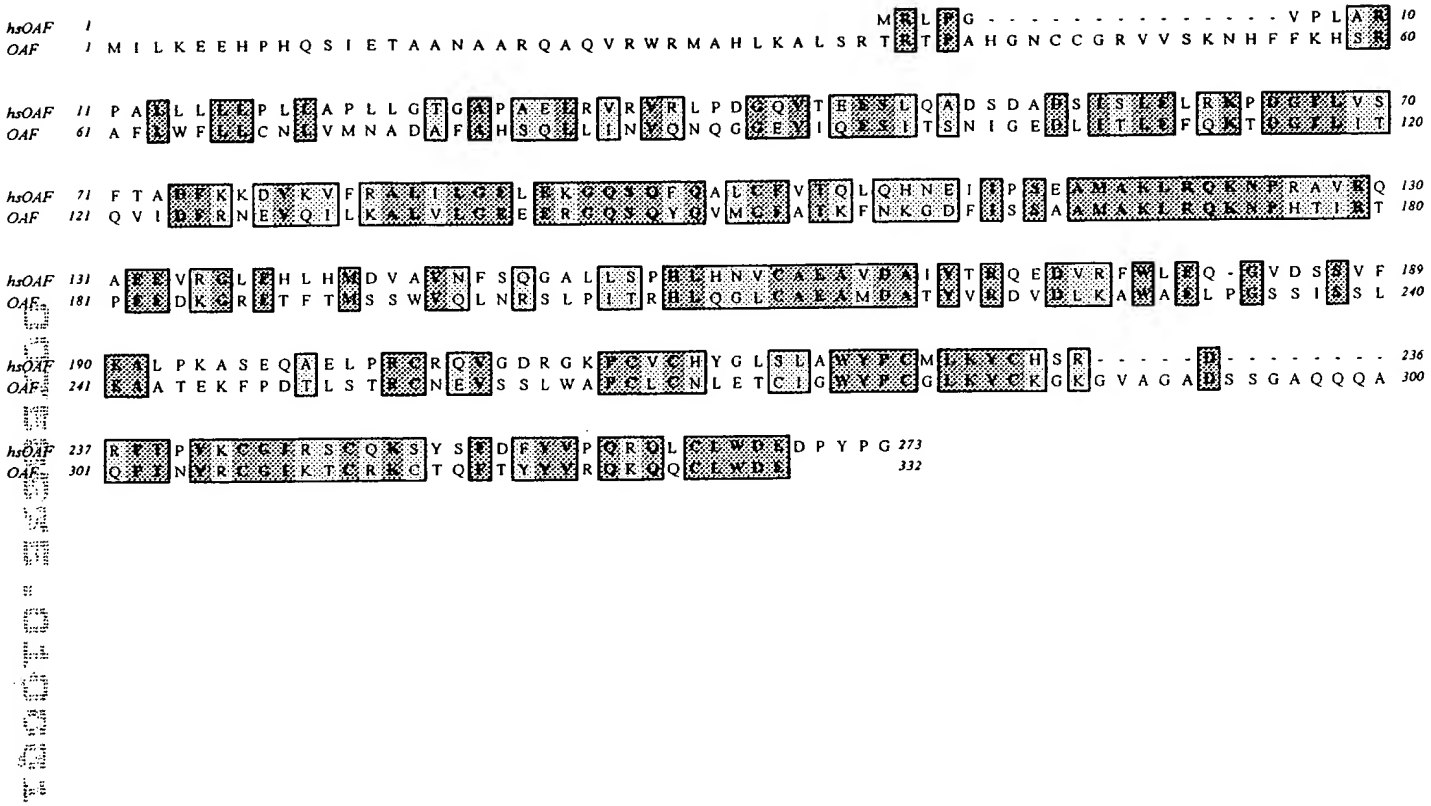


FIGURE 8A

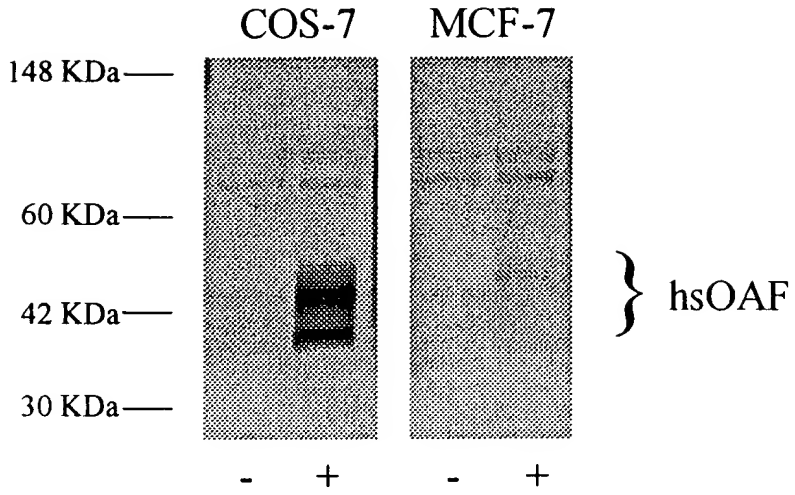


FIGURE 8B

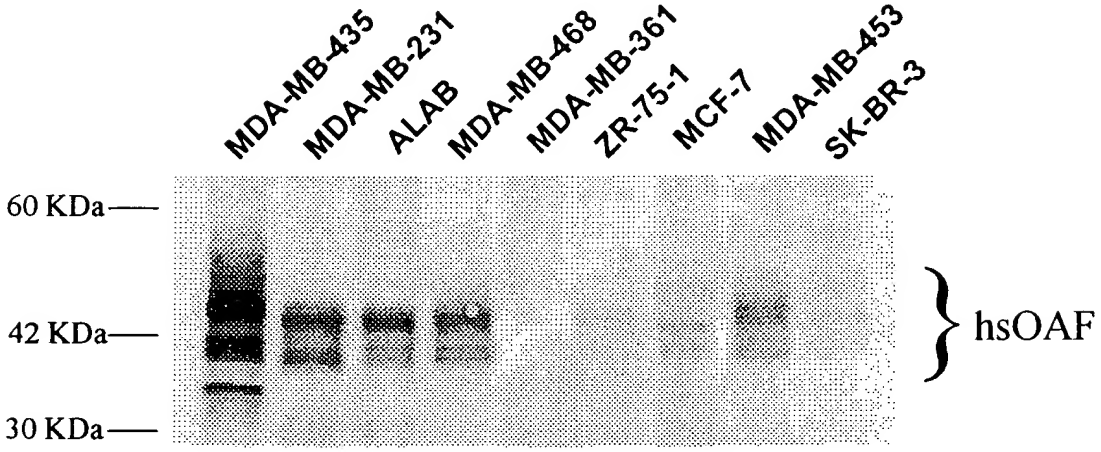


FIGURE 9

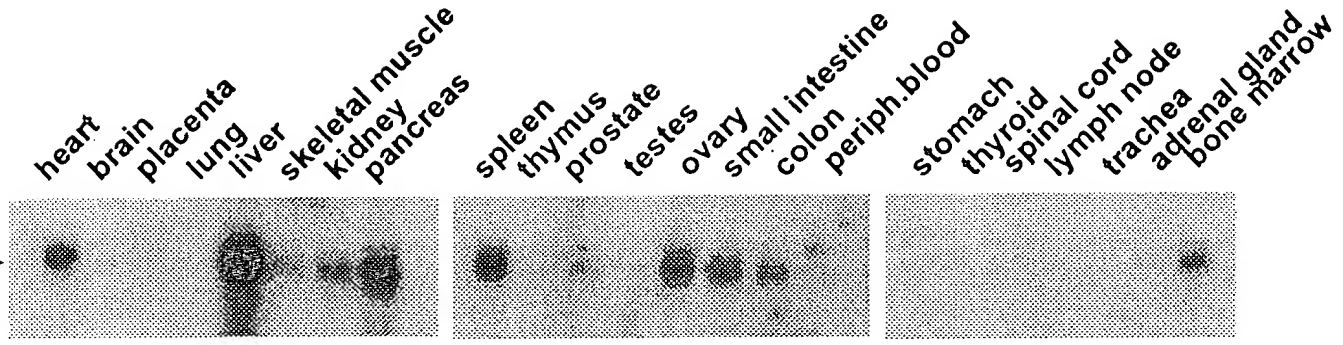
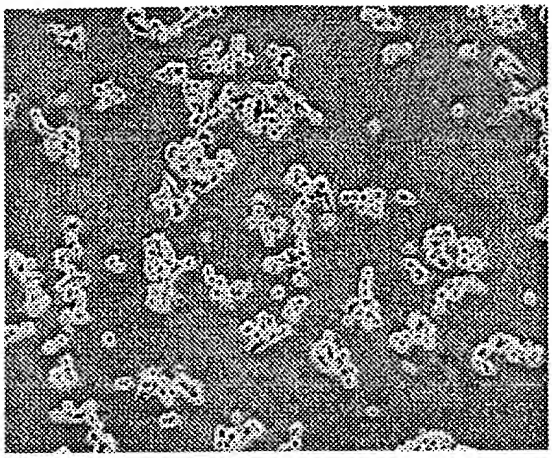
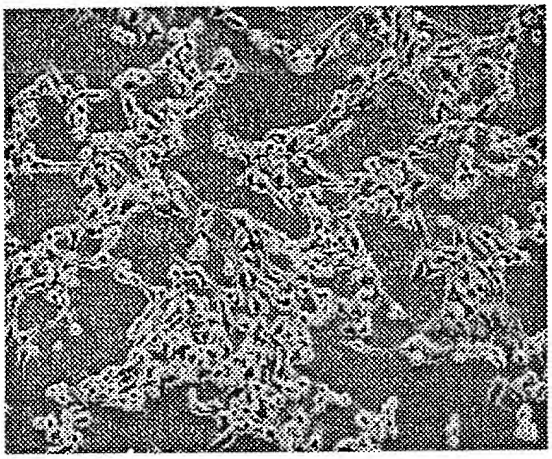

heart
brain
placenta
lung
liver
skeletal muscle
kidney
pancreas
spleen
thymus
prostate
testes
ovary
small intestine
colon
periph.blood
stomach
thyroid
spinal cord
lymph node
trachea
adrenal gland
bone marrow

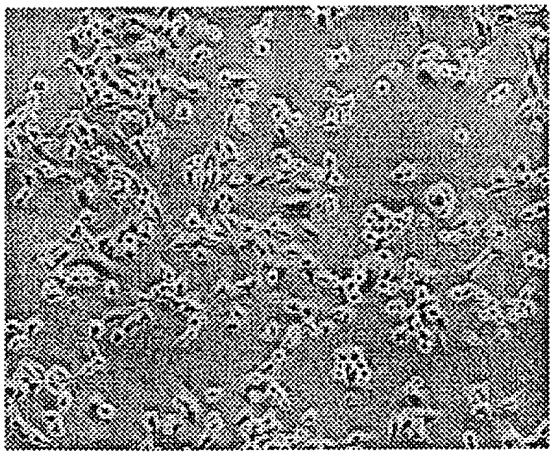
FIGURE 10A



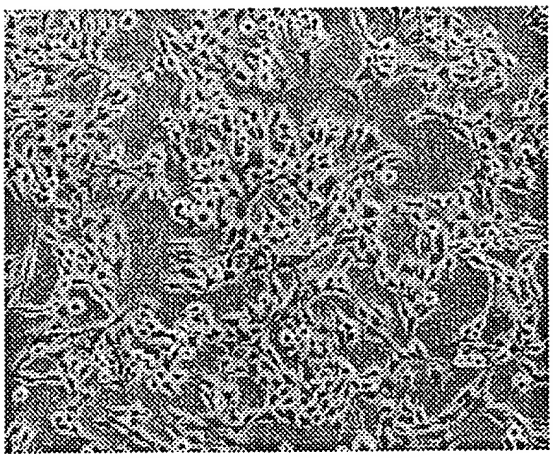
AS



RC

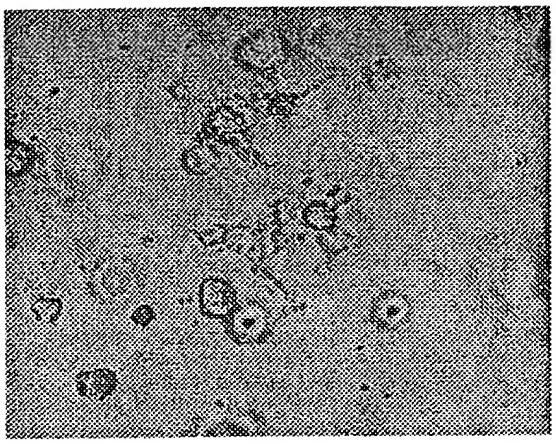


AS+M

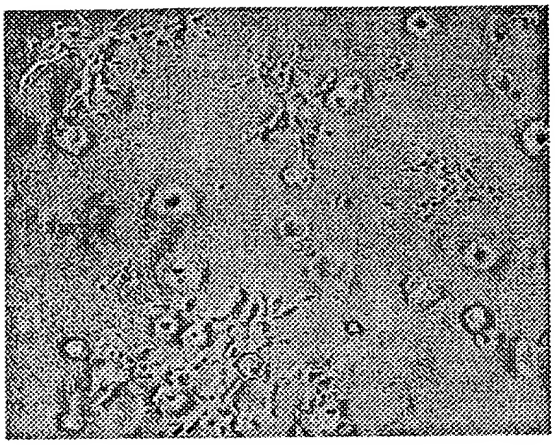


Normal

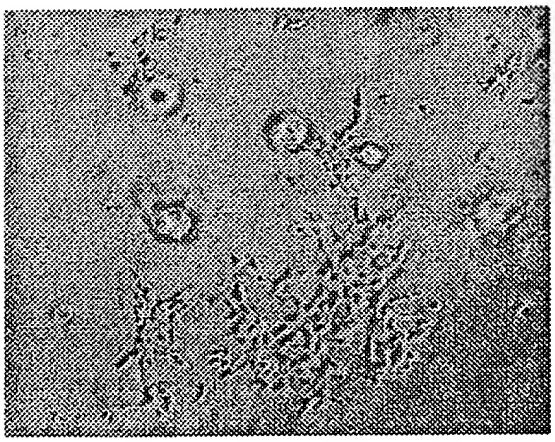
FIGURE 10B



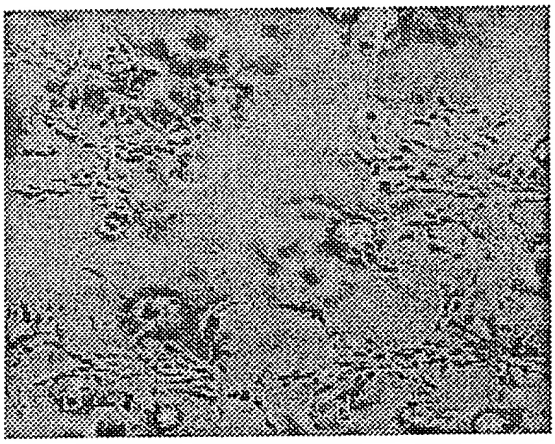
AS



RC



AS+M



Normal

FIGURE 11

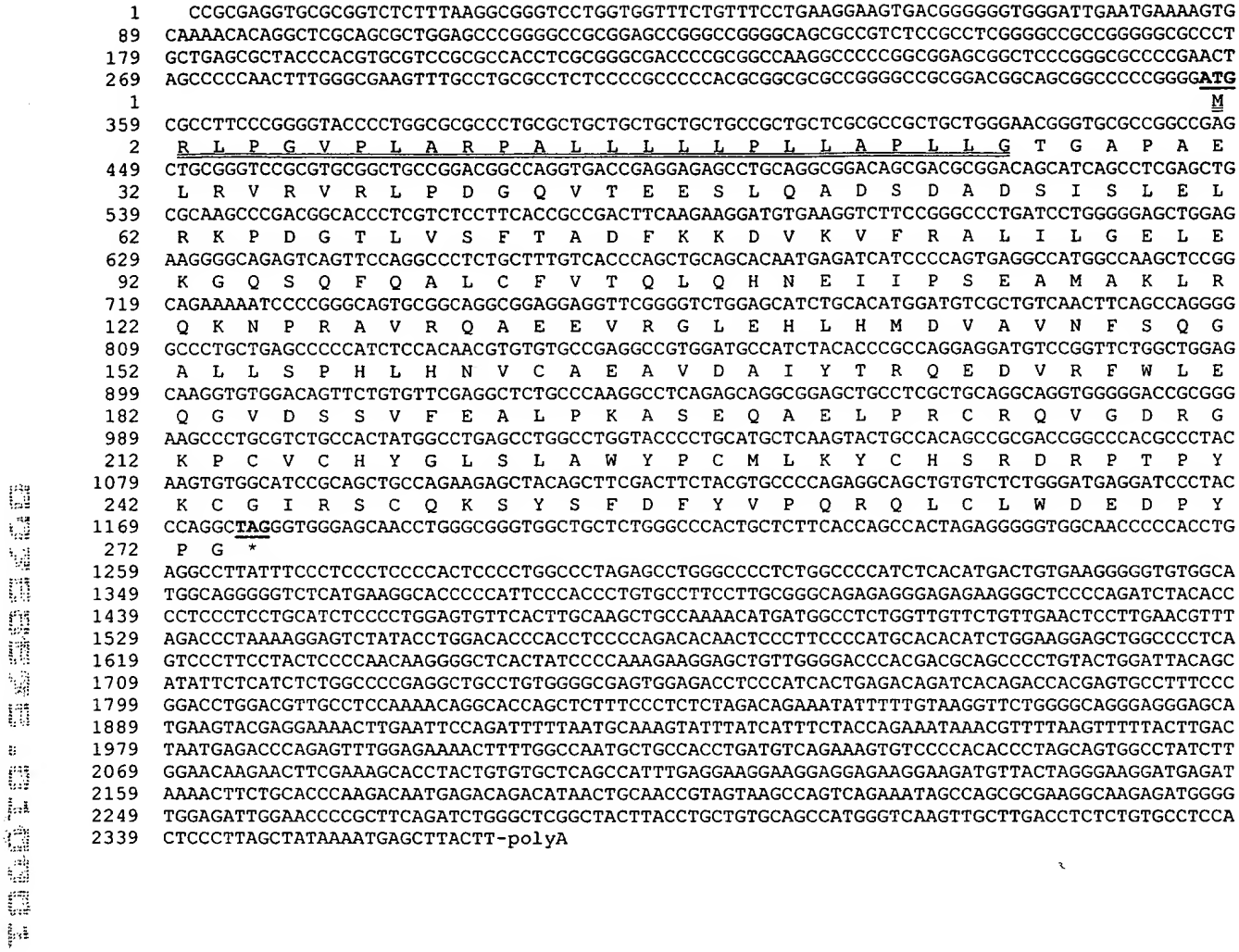

1 CCGCGAGGTGCGCGGTCTCTTTAAGGCGGGTCCTGGTGGTTTCTGTTTCCTGAAGGAAGTGACGGGGGGTGGGATTGAATGAAAAGTG
89 CAAAACACAGGCTCGCAGCGCTGGAGCCCGGGGCCGCGGAGCCGGGCCGGGGCAGCGCCGTCTCCGCCTCGGGGCCGCCGGGGGCGCCCT
179 GCTGAGCGCTACCCACGTGCGTCCGCGCCACCTCGCGGGCGACCCCGCGGCCAAGGCCCCCGGCGGAGCGGCTCCCGGGCGCCCCGAACT
269 AGCCCCCAACTTTGGGCGAAGTTTGCCTGCGCCTCTCCCCGCCCCCACGCGGCGCGCCGGGGCCGCGGACGGCAGCGGCCCCCGGGGATG
1 M
359 CGCCTTCCCGGGGTACCCCTGGCGCGCCCTGCGCTGCTGCTGCTGCTGCCGCTGCTCGCGCCGCTGCTGGGAACGGGTGCGCCGGCCGAG
2 R L P G V P L A R P A L L L L L P L L A P L L G T G A P A E
449 CTGCGGGTCCGCGTGCGGCTGCCGGACGGCCAGGTGACCGAGGAGAGCCTGCAGGCGGACAGCGACGCGGACAGCATCAGCCTCGAGCTG
32 L R V R V R L P D G Q V T E E S L Q A D S D A D S I S L E L
539 CGCAAGCCCGACGGCACCCTCGTCTCCTTCACCGCCGACTTCAAGAAGGATGTGAAGGTCTTCCGGGCCCTGATCCTGGGGGAGCTGGAG
62 R K P D G T L V S F T A D F K K D V K V F R A L I L G E L E
629 AAGGGGCAGAGTCAGTTCCAGGCCCTCTGCTTTGTCACCCAGCTGCAGCACAATGAGATCATCCCCAGTGAGGCCATGGCCAAGCTCCGG
92 K G Q S Q F Q A L C F V T Q L Q H N E I I P S E A M A K L R
719 CAGAAAAATCCCCGGGCAGTGCGGCAGGCGGAGGAGGTTCGGGGTCTGGAGCATCTGCACATGGATGTCGCTGTCAACTTCAGCCAGGGG
122 Q K N P R A V R Q A E E V R G L E H L H M D V A V N F S Q G
809 GCCCTGCTGAGCCCCCATCTCCACAACGTGTGTGCCGAGGCCGTGGATGCCATCTACACCCGCCAGGAGGATGTCCGGTTCTGGCTGGAG
152 A L L S P H L H N V C A E A V D A I Y T R Q E D V R F W L E
899 CAAGGTGTGGACAGTTCTGTGTTCGAGGCTCTGCCCAAGGCCTCAGAGCAGGCGGAGCTGCCTCGCTGCAGGCAGGTGGGGGACCGCGGG
182 Q G V D S S V F E A L P K A S E Q A E L P R C R Q V G D R G
989 AAGCCCTGCGTCTGCCACTATGGCCTGAGCCTGGCCTGGTACCCCTGCATGCTCAAGTACTGCCACAGCCGCGACCGGCCCACGCCCTAC
212 K P C V C H Y G L S L A W Y P C M L K Y C H S R D R P T P Y
1079 AAGTGTGGCATCCGCAGCTGCCAGAAGAGCTACAGCTTCGACTTCTACGTGCCCCAGAGGCAGCTGTGTCTCTGGGATGAGGATCCCTAC
242 K C G I R S C Q K S Y S F D F Y V P Q R Q L C L W D E D P Y
1169 CCAGGCTAGGGTGGGAGCAACCTGGGCGGGTGGCTGCTCTGGGCCCACTGCTCTTCACCAGCCACTAGAGGGGGTGGCAACCCCCACCTG
272 P G *
1259 AGGCCTTATTTCCCTCCCTCCCCACTCCCCTGGCCCTAGAGCCTGGGCCCCTCTGGCCCCATCTCACATGACTGTGAAGGGGGTGTGGCA
1349 TGGCAGGGGGTCTCATGAAGGCACCCCCATTCCCACCCTGTGCCTTCCTTGCGGGCAGAGAGGGAGAGAAGGGCTCCCCAGATCTACACC
1439 CCTCCCTCCTGCATCTCCCCTGGAGTGTTCACTTGCAAGCTGCCAAAACATGATGGCCTCTGGTTGTTCTGTTGAACTCCTTGAACGTTT
1529 AGACCCTAAAAGGAGTCTATACCTGGACACCCACCTCCCCAGACACAACTCCCTTCCCCATGCACACATCTGGAAGGAGCTGGCCCCTCA
1619 GTCCCTTCCTACTCCCCAACAAGGGGCTCACTATCCCCAAAGAAGGAGCTGTTGGGGACCCACGACGCAGCCCCTGTACTGGATTACAGC
1709 ATATTCTCATCTCTGGCCCCGAGGCTGCCTGTGGGGCGAGTGGAGACCTCCCATCACTGAGACAGATCACAGACCACGAGTGCCTTTCCC
1799 GGACCTGGACGTTGCCTCCAAAACAGGCACCAGCTCTTTCCCTCTCTAGACAGAAATATTTTTGTAAGGTTCTGGGGCAGGGAGGGAGCA
1889 TGAAGTACGAGGAAAACTTGAATTCCAGATTTTTAATGCAAAGTATTTATCATTTCTACCAGAAATAAACGTTTTAAGTTTTTACTTGAC
1979 TAATGAGACCCAGAGTTTGGAGAAAACTTTTGGCCAATGCTGCCACCTGATGTCAGAAAGTGTCCCCACACCCTAGCAGTGGCCTATCTT
2069 GGAACAAGAACTTCGAAAGCACCTACTGTGTGCTCAGCCATTTGAGGAAGGAAGGAGGAGAAGGAAGATGTTACTAGGGAAGGATGAGAT
2159 AAAACTTCTGCACCCAAGACAATGAGACAGACATAACTGCAACCGTAGTAAGCCAGTCAGAAATAGCCAGCGCGAAGGCAAGAGATGGGG
2249 TGGAGATTGGAACCCCGCTTCAGATCTGGGCTCGGCTACTTACCTGCTGTGCAGCCATGGGTCAAGTTGCTTGACCTCTCTGTGCCTCCA
2339 CTCCCTTAGCTATAAAATGAGCTTACTT-polyA

FIGURE 12A

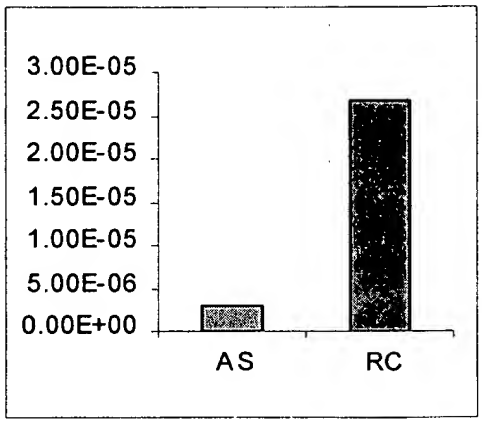


FIGURE 12B